SEQUENCE LISTING

<110> CHUGAI SEIYAKU KABUSIKI KAISHA

<120> Vascularization Inhibitors

<130> CGS-I 98-06 PCT

<140> PCT/JP99/01448
<141> 1999-03-23

<150> JP10/95448
<151> 1998-03-24

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Glu Glu Asn Ala Asn Phe Asn Lys Ile Phe Leu Pro Thr Ile Tyr
                    35                  40                  45
Ser Ile Ile Phe Leu Thr Gly Ile Val Gly Asn Gly Leu Val Ile
                    50                  55                  60
Leu Val Met Gly Tyr Gln Lys Lys Leu Arg Ser Met Thr Asp Lys
                    65                  70                  75
Tyr Arg Leu His Leu Ser Val Ala Asp Leu Leu Phe Val Ile Thr
                    80                  85                  90
Leu Pro Phe Trp Ala Val Asp Ala Val Ala Asn Trp Tyr Phe Gly
                    95                  100                 105
Asn Phe Leu Cys Lys Ala Val His Val Ile Tyr Thr Val Asn Leu
                    110                 115                 120
Tyr Ser Ser Val Leu Ile Leu Ala Phe Ile Ser Leu Asp Arg Tyr
                    125                 130                 135
Leu Ala Ile Val His Ala Thr Asn Ser Gln Arg Pro Arg Lys Leu
                    140                 145                 150
Leu Ala Glu Lys Val Val Tyr Val Gly Val Trp Ile Pro Ala Leu
                    155                 160                 165
Leu Leu Thr Ile Pro Asp Phe Ile Phe Ala Asn Val Ser Glu Ala
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               170                    175                    180
     Asp Asp Arg Tyr Ile Cys Asp Arg Phe Tyr Pro Asn Asp Leu Trp
               185                    190                    195
     Val Val Val Phe Gln Phe Gln His Ile Met Val Gly Leu Ile Leu
               200                    205                    210
     Pro Gly Ile Val Ile Leu Ser Cys Tyr Cys Ile Ile Ile Ser Lys
               215                    220                    225
     Leu Ser His Ser Lys Gly His Gln Lys Arg Lys Ala Leu Lys Thr
               230                    235                    240
     Thr Val Ile Leu Ile Leu Ala Phe Phe Ala Cys Trp Leu Pro Tyr
               245                    250                    255
     Tyr Ile Gly Ile Ser Ile Asp Ser Phe Ile Leu Leu Glu Ile Ile
               260                    265                    270
     Lys Gln Gly Cys Glu Phe Glu Asn Thr Val His Lys Trp Ile Ser
               275                    280                    285
     Ile Thr Glu Ala Leu Ala Phe Phe His Cys Cys Leu Asn Pro Ile
               290                    295                    300
     Leu Tyr Ala Phe Leu Gly Ala Lys Phe Lys Thr Ser Ala Gln His
               305                    310                    315
     Ala Leu Thr Ser Val Ser Arg Gly Ser Ser Leu Lys Ile Leu Ser
               320                    325                    330
     Lys Gly Lys Arg Gly Gly His Ser Ser Val Ser Thr Glu Ser Glu
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     Ser Ser Ser Phe His Ser Ser
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<211> 1588
<212> DNA
<213> Mus


<220>
<221> CDS
<222> (1)...(1059)


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gaa gaa aat gct aat ttc aat aaa atc ttc ctg ccc acc atc tac   135
tcc atc atc ttc tta act ggc att gtg ggc aat gga ttg gtc atc   180
ctg gtc atg ggt tac cag aag aaa ctg aga agc atg acg gac aag   225
tac agg ctg cac ctg tca gtg gcc gac ctc ctc ttt gtc atc acg   270
ctt ccc ttc tgg gca gtt gat gcc gtg gca aac tgg tac ttt ggg   315
aac ttc cta tgc aag gca gtc cat gtc atc tac aca gtc aac ctc   360
tac agc agt gtc ctc atc ctg gcc ttc atc agt ctg gac cgc tac   405
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ctg gcc atc gtc cac gcc acc aac agt cag agg cca agg aag ctg 450
ttg gct gaa aag gtg gtc tat gtt ggc gtc tgg atc cct gcc ctc 495
ctg ctg act att ccc gac ttc atc ttt gcc aac gtc agt gag gca 540
gat gac aga tat atc tgt gac cgc ttc tac ccc aat gac ttg tgg 585
gtg gtt gtg ttc cag ttt cag cac atc atg gtt ggc ctt atc ctg 630
cct ggt att gtc atc ctg tcc tgc tat tgc att atc atc tcc aag 675
ctg tca cac tcc aag ggc cac cag aag cgc aag gcc ctc aag acc 720
aca gtc atc ctc atc ctg gct ttc ttc gcc tgt tgg ctg cct tac 765
tac att ggg atc agc atc gac tcc ttc atc ctc ctg gaa atc atc 810
aag caa ggg tgt gag ttt gag aac act gtg cac aag tgg att tcc 855
atc acc gag gcc cta gct ttc ttc cac tgt tgt ctg aac ccc atc 900
ctc tat gct ttc ctt gga gcc aaa ttt aaa acc tct gcc cag cac 945
gca ctc acc tct gtg agc aga ggg tcc agc ctc aag atc ctc tcc 990
aaa gga aag cga ggt gga cat tca tct gtt tcc act gag tct gag 1035
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aattgactta tttatataaa ttttttttgt ttcatattga tgtgtgtcta ggcaggacct 1265
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gataatctct ccattcccgt ggaacgtttt tcctgttctt aagacgtgat tttgctgtag 1445
aagatggcac ttataaccaa agcccaaagt ggtatagaaa tgctggtttt tcagttttca 1505
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<211> 359
<212> PRT
<213> Mus

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Glu Glu Val Gly Ser Gly Asp Tyr Asp Ser Asn Lys Glu Pro Cys
                 20                  25                  30
Phe Arg Asp Glu Asn Val His Phe Asn Arg Ile Phe Leu Pro Thr
                 35                  40                  45
Ile Tyr Phe Ile Ile Phe Leu Thr Gly Ile Val Gly Asn Gly Leu
                 50                  55                  60
Val Ile Leu Val Met Gly Tyr Gln Lys Lys Leu Arg Ser Met Thr
                 65                  70                  75
Asp Lys Tyr Arg Leu His Leu Ser Val Ala Asp Leu Leu Phe Val
                 80                  85                  90
Ile Thr Leu Pro Phe Trp Ala Val Asp Ala Met al.a Asp Trp Tyr
                 95                 100                 105
```

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Phe Gly Lys Phe Leu Cys Lys Ala Val His Ile Ile Tyr Thr Val
              110                     115                     120
Asn Leu Tyr Ser Ser Val Leu Ile Leu Ala Phe Ile Ser Leu Asp
              125                     130                     135
Arg Tyr Leu Ala Ile Val His Ala Thr Asn Ser Gln Arg Pro Arg
              140                     145                     150
Lys Leu Leu Ala Glu Lys Ala Val Tyr Val Gly Val Trp Ile Pro
              155                     160                     165
Ala Leu Leu Leu Thr Ile Pro Asp Phe Ile Phe Ala Asp Val Ser
              170                     175                     180
Gln Gly Asp Ile Ser Gln Gly Asp Asp Arg Tyr Ile Cys Asp Arg
              185                     190                     195
Leu Tyr Pro Asp Ser Leu Trp Met Val Val Phe Gln Phe Gln His
              200                     205                     210
Ile Met Val Gly Leu Ile Leu Pro Gly Ile Val Ile Leu Ser Cys
              215                     220                     225
Tyr Cys Ile Ile Ile Ser Lys Leu Ser His Ser Lys Gly His Gln
              230                     235                     240
Lys Arg Lys Ala Leu Lys Thr Thr Val Ile Leu Ile Leu Ala Phe
              245                     250                     255
Phe Ala Cys Trp Leu Pro Tyr Tyr Val Gly Ile Ser Ile Asp Ser
              260                     265                     270
Phe Ile Leu Leu Gly Val Ile Lys Gln Gly Cys Asp Phe Glu Ser
              275                     280                     285
Ile Val His Lys Trp Ile Ser Ile Thr Glu Ala Leu Ala Phe Phe
              290                     295                     300
His Cys Cys Leu Asn Pro Ile Leu Tyr Ala Phe Leu Gly Ala Lys
              305                     310                     315
Phe Lys Ser Ser Ala Gln His Ala Leu Asn Ser Met Ser Arg Gly
              320                     325                     330
Ser Ser Leu Lys Ile Leu Ser Lys Gly Lys Arg Gly Gly His Ser
              335                     340                     345
Ser Val Ser Thr Glu Ser Glu Ser Ser Ser Phe His Ser Ser
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<211> 1758
<212> DNA
<213> Mus

<220>
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<222> (1)...(1080)
<223>
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ttc cgg gat gaa aac gtc cat ttc aat agg atc ttc ctg ccc acc 135
atc tac ttc atc atc ttc ttg act ggc ata gtc ggc aat gga ttg 180
gtg atc ctg gtc atg ggt tac cag aag aag cta agg agc atg acg 225
gac aag tac cgg ctg cac ctg tca gtg gct gac ctc ctc ttt gtc 270
atc aca ctc ccc ttc tgg gca gtt gat gcc atg gct gac tgg tac 315
ttt ggg aaa ttt ttg tgt aag gct gtc cat atc atc tac act gtc 360
aac ctc tac agc agc gtt ctc atc ctg gcc ttc atc agc ctg gac 405
cgg tac ctc gcc att gtc cac gcc acc aac agt caa agg cca agg 450
aaa ctg ctg gct gaa aag gca gtc tat gtg ggc gtc tgg atc cca 495
gcc ctc ctc ctg act ata cct gac ttc atc ttt gcc gac gtc agc 540
cag ggg gac atc agt cag ggg gat gac agg tac atc tgt gac cgc 585
ctt tac ccc gat agc ctg tgg atg gtg gtg ttt caa ttc cag cat 630
ata atg gtg ggt ctc atc ctg ccc ggc atc gtc atc ctc tcc tgt 675
tac tgc atc atc atc tct aag ctg tca cac tcc aag ggc cac cag 720
aag cgc aag gcc ctc aag acg aca gtc atc ctc atc cta gct ttc 765
ttt gcc tgc tgg ctg cca tat tat gtg ggg atc agc atc gac tcc 810
ttc atc ctt ttg gga gtc atc aag caa gga tgt gac ttc gag agc 855
att gtg cac aag tgg atc tcc atc aca gag gcc ctc gcc ttc ttc 900
cac tgt tgc ctg aac ccc atc ctc tat gcc ttc ctc ggg gcc aag 945
ttc aaa agc tct gcc cag cat gca ctc aac tcc atg agc aga ggc 990
tcc agc ctc aag atc ctt tcc aaa gga aag cgg ggt gga cac tct 1035
tcc gtc tcc acg gag tca gaa tcc tcc agt ttt cac tcc agc taa 1080
cccttatgca aagacttata taatatatat atatatatga taaagaactt ttttatgtta 1140
cacattttcc agatataaga gactgaccag tcttgtacag ttttttttttt tttttaattg 1200
actgttggga gtttatgttc ctctagtttt tgtgaggttt gacttaattt atataaatat 1260
tgttttttgt ttgtttcatg tgaatgagcg tctaggcagg acctgtggcc aagttcttag 1320
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aagatggcac ttaaaaccaa agcctgaaat ggtggtagaa atgctggggt tttttttgtt 1620
tgtttgtttt ttcagttttc aagagtagat tgacttcagt ccctacaaat gtacagtctt 1680
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<210> 5
<211> 89
<212> PRT
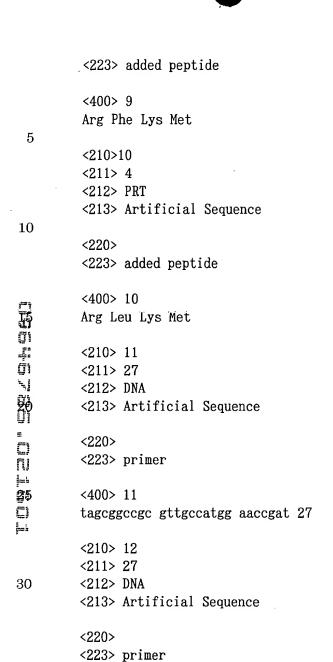<213> Artificial Sequence

<223> Ligand peptide

<400> 5
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Leu Cys Leu Ser Asp Gly Lys Pro Val Ser Leu Ser Tyr Arg Cys
                    20                  25                  30
Pro Cys Arg Phe Phe Glu Ser His Val Ala Arg Ala Asn Val Lys
                    35                  40                  45
His Leu Lys Ile Leu Asn Thr Pro Asn Cys Ala Leu Gln Ile Val
                    50                  55                  60
Ala Arg Leu Lys Asn Asn Asn Arg Gln Val Cys Ile Asp Pro Lys
                    65                  70                  75
Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys Ala Leu Asn Lys
                    80                  85
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<210> 6
<211> 2244
<212> DNA
<213> Mus

<220>
<221> CDS
<222> (471)...(743)

<400> 6
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ggaggcacgg ggcctggagg cgccaggcgg aggatgcggg cgacacggtg gcggcggcga  180
ccgcgcgacc gggcgggcgg gcgggcaggg gcgagcggag ggagggagcg gactgcggca  240
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cgccgctccc ctccagctcg cctgcgcctc tcactctccg tcagccgcat tgcccgctcg  420
gcgtccggcc cccgacccgc gctcgtccgc ccgccgccc gcccgcccgc gcc  473
atg aac gcc aag gtc gtg gtc gtg ctg gtc ctc gtg ctg acc gcg  518
ctc tgc ctc agc gac ggg aag ccc gtc agc ctg agc tac aga tgc  563
cca tgc cga ttc ttc gaa agc cat gtt gcc aga gcc aac gtc aag  608
cat ctc aaa att ctc aac act cca aac tgt gcc ctt cag att gta  653
gcc cgg ctg aag aac aac aac aga caa gtg tgc att gac ccg aag  698
cta aag tgg att cag gag tac ctg gag aaa gct tta aac aag taa  743
gcacaacagc caaaaaggac tttccgctag acccactcga ggaaactaa aaccttgtga  803
gagatgaaag ggcaaagacg tggggaggg ggccttaacc atgaggacca ggtgtgtgtg  863
tggggtgggc acattgatct gggatcgggc ctgaggtttg ccagcattta gaccctgcat  923
ttatagcata cggtatgata ttgcagctta tattcatcca tgccctgtac ctgtgcacgt  983
tggaattttt attactgggg tttttctaag aaagaaattg tattatcaac agcattttca 1043
agcagttagt tccttcatga tcatcacaat catcatcatt ctcattctca ttttttaaat 1103
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atttcaaaat atatttatag tcgaacaatt catatatttg aagtggagcc atatgaatgt 2063
cagtagttta tacttctcta ttatctcaaa ctactggcaa tttgtaaaga aatatatatg 2123
atatataaat gtgattgcag ctttctcaatg ttagccacag tgtattttt cacttgtact 2183
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<210> 7
<211> 89
<212> PRT
<213> Artificial Sequence

<223> Ligand peptide

<400> 7

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Leu Cys Ile Ser Asp Gly Lys Pro Val Ser Leu Ser Tyr Arg Cys
                20                  25                  30
Pro Cys Arg Phe Phe Glu Ser His Ile Ala Arg Ala Asn Val Lys
                35                  40                  45
His Leu Lys Ile Leu Asn Thr Pro Asn Cys Ala Leu Gln Ile Val
                50                  55                  60
Ala Arg Leu Lys Asn Asn Asn Arg Gln Val Cys Ile Asp Pro Lys
                65                  70                  75
Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys Ala Leu Asn Lys
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<210> 8
<211> 1781
<212> DNA
<213> Mua

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<220>
<221> CDS
<222> (82)...(351)

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ctc tgc atc agt gac ggt aaa cca gtc agc ctg agc tac cga tgc        171
ccc tgc cgg ttc ttc gag agc cac atc gcc aga gcc aac gtc aag        216
cat ctg aaa atc ctc aac act cca aac tgt gcc ctt cag att gtt        261
gca cgg ctg aag aac aac aac aga caa gtg tgc att gac ccg aaa        306
tta aag tgg atc caa gag tac ctg gag aaa gct tta aac aag taa        351
gcacaacagc ccaaaggact ttccagtaga cccccgagga aggctgacat ccgtgggaga  411
tgcaagggca gtggtgggga ggagggcctg aaccctggcc aggatggccg gcgggacagc  471
actgactggg gtcatgctaa ggtttgccag cataaagaca ctccgccata gcatatggta  531
cgatattgca gcttatattc atccctgccc tcgcccgtgc acaatggagc ttttataact  591
ggggtttttc taaggaattg tattacccta accagttagc ttcatcccca ttctcctcat  651
cctcatcttc attttaaaaa gcagtgatta cttcaagggc tgtattcagt ttgctttgga  711
gcttctcttt gccctggggc ctctgggcac agttatagac ggtggctttg cagggagccc  771
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ctttatccag ttcagtgcca gggtcgggaa gcttccttta gaagtgatcc ctgaagctgt  951
gctcagagac cctttcctag ccgttcctgc tctctgcttg cctccaaacg catgcttcat  1011
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agtgatgtgg ggtgccccct ccctctcttc cctttgcttt cctctcactt gggccctttg  1131
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gctctgatcg aatatcagtg atgaaaataa taataataat aataataacg aataagccag  1371
aatcttgcca tgaagccaca gtggggattc tgggttccaa tcagaaatgg agacaagata  1431
aaacttgcat acattcttat gatcacagac ggccctggtg gtttttggta actatttaca  1491
aggcattttt ttacatatat ttttgtgcac tttttatgtt tctttggaag acaaatgtat  1551
ttcagaatat atttgtagtc aattcatata tttgaagtgg agccatagta atgccagtag  1611
atatctctat gatcttgagc tactggcaac ttgtaaagaa atatatatga catataaatg  1671
tattgtagct ttccggtgtc agccacggtg tattttttcca cttggaatga aattgtatca  1731
actgtgacat tatatgcact agcaataaaa tgctaattgt ttcatgctgt             1781


<210> 9
<211> 4
<212> PRT
<213> Artificial Sequence


<220>
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.<223> added peptide

<400> 9
Arg Phe Lys Met

<210>10
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> added peptide

<400> 10
Arg Leu Lys Met

<210> 11
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 11
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<210> 12
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 12
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